REMARKS

Following entry of the present amendment, claims 37-214 will be pending in the application, claims 1-36 having been cancelled and new claims 37-214 added. Support for new claims 37-45, 73-84, 100-123, 133-144, 150-173, 183-194 and 200-214 can be found in the specification at, for example, pages 17-18, 58, 59 and 62-68. Support for new claims 46-63, 85-94, 124-132, 145-149, 174-182 and 195-199, can be found, e.g., in Examples 14 and 15 of the specification. Support for new claims 64-72 and 95-99 can be found, e.g., in Example 15 of the specification. The specification is amended to correct certain typographical and grammatical errors. The abstract and title have been replaced. No new matter has been added.

Applicants thank the Examiner for the very courteous and helpful interviews on April 3, 2002 (in person), and July 11 and 16, 2002 (by telephone), during which the claims and possible amendments thereto were discussed. The Examiner's thorough preparation for those interviews is particularly appreciated. The above amendments reflect the substance of the agreements reached in those interviews concerning claim language.

The Office Action dated January 17, 2002, noted that English language translations of the Japanese priority documents had not been filed as of that date. Applicants subsequently submitted such translations on April 18, 2002.

As requested in the Office Action, the abstract and title have been amended above and new formal drawings submitted (under separate cover). The noted hyperlink has been removed.

Various informalities in the claims are noted on page 3 of the Office Action. It is believed that the above amendments resolve these informalities.

The rejection of claim 27 under 35 USC 101 is obviated by the cancellation of claim 27 and the inclusion of the term "isolated" in the new claims, as suggested by the Examiner.

The various rejections of claims 27-34 under 35 USC 112, second paragraph, are fully addressed by the amended claims presented above.

The various rejections of claims 27-34 under 35 USC 112, first paragraph, for lack of written description and enablement are fully addressed by the amended claims presented above.

The rejection of claims 27-34 as anticipated by Hutloff et al. under 35 USC 102(a) is obviated by the amended claims presented above, none of which is anticipated by the antibody of Hutloff et al.

The rejection of claims 27-34 under 35 USC 102(b) as anticipated by Redoglia et al. as evidenced by Buonfiglio et al. and Mages et al. is obviated by the amended claims presented above, none of which is anticipated by the antibody of Redoglia et al.

In view of the amended claims presented above, withdrawal of the statutory double patenting rejection on page 11 of the Office Action is respectfully requested.

Applicants wish to bring to the examiner's attention USSN 09/859,053, assigned to the same entity as the present application.

Attached is a marked-up version of the changes being made by the current amendment.

Applicants ask that all claims be allowed. A three-month extension of time for filing this response is respectfully requested. Please apply the amounts of $3,060 for excess claim fees and $920 for the Three-Month Petition for Extension of Time fee, as well as any other charges or credits, to Deposit Account No. 06-1050, referencing Attorney Docket No. 06501-039001.

Respectfully submitted,

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Version with markings to show changes made

In the title:

The title at page 1, line 1, has been amended as follows:

ANTIBODIES SPECIFIC FOR A CELL SURFACE MOLECULE MEDIATING CELL ADHESION AND SIGNAL TRANSMISSION, CELLS SECRETING SUCH ANTIBODIES, AND METHODS OF MAKING AND USING SUCH ANTIBOIDES

In the specification:

The paragraph beginning at page 5, line 1, has been amended as follows:

The ligands for CD28 and CTLA-4 are CD80 (B7-1) and CD86 (B7-2) in human and mice. CTLA-4 has about 20 times [as] higher affinity to both ligands as CD28. It has been elucidated that the amino acid sequence structures "MYPPPY (Met-Tyr-Pro-Pro-Pro-Tyr)" (SEQ ID NO:18) conserved through animal species is important for the binding of CD28 and CTLA-4 to CD80 (B7-1). It has also been reported that, when CD28 is stimulated, PI3 kinase (phosphoinositide 3 kinase, PI3K) associates with the phosphorylated tyrosine residue in a partial sequence "YMNM (Tyr-Met-Asn-Met)" (SEQ ID NO:19) of CD28 ["YMNM (Tyr-Met-Asn-Met)" (SEQ ID NO:19)] and that CD28 plays an important role in intracellular signal transmission through this "YxxM" structure. Furthermore, it has been reported that CTLA-4 also has a sequence represented by "YxxM," namely "YVKM (Tyr-Val-Lys-Met)" (SEQ ID NO:20) in its cytoplasmic region and that, after being stimulated, SYP associates with this sequence.

The paragraph beginning at page 34, line 3, has been amended as follows:

To determine percent homology between two sequences, the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5877 is used. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST nucleotide searches are performed with the NBLAST program, score = 100, word

length = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches are performed with the XBLAST program, score = 50, word length = 3 to obtain amino acid sequences homologous to a VRK1 or VRK2 protein molecules. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (1997) Nucleic Acids Res. 25:3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. [See http://www.ncbi.nlm.nih.gov] See, web site of National Center for Biotechnology Information (NCBI), which is a division of National Library of Medicine (NLM) at the National Institute of Health (NIH) in USA.

The paragraph beginning at page 84, line 4, has been amended as follows:

After the purified "JTT-1 antigen" was subjected to SDS-PAGE, the N-terminal amino acid sequence was determined by the usual method. The result revealed that "JTT-1 antigen" contained an amino acid sequence Glu-Leu-Asn-Asp-Leu-Ala-Asn-His-Arg (amino acid residues 21-29 of SEQ ID NO:13).

The paragraph beginning at page 88, line 4, has been amended as follows:

The nucleotide sequence of clone "T132A7" was determined by dideoxy method with "Auto Read Sequencing Kit" (Pharmacia) and "A.L.F. DNA Sequencer" (Pharmacia). In addition, the deduced amino acid sequence of "rat JTT-1 antigen" encoded by the nucleotide sequence was analyzed with gene analysis software "GENEWORKS" (IntelliGenetics). The nucleotide sequence and the deduced amino acid sequence [were] are shown in SEQ ID NO:4 and SEQ ID NO:13, respectively.

The paragraph beginning at page 94, line 10, has been amended as follows:

The nucleotide sequence[s] of each of the five clones [were] was determined by dideoxy method with "Auto Read Sequencing Kit" (Pharmacia) and "A.L.F. DNA Sequencer" (Pharmacia). [The four] Four of the five clones comprise the same nucleotide sequence. The

nucleotide sequence of cDNA encoding the full length of "mouse JTT-1 antigen" and the deduced amino acid sequence are shown in SEQ ID NO:5 and SEQ ID NO:14, respectively.

The paragraph beginning at page 97, line 22, has been amended as follows:

The nucleotide sequences of the two clones were determined by the dideoxy method with an "Auto Read Sequencing Kit" (Pharmacia) and A.L.F. DNA Sequencer (Pharmacia). The two clones comprise the same nucleotide sequence. The nucleotide sequence of cDNA encoding the full length of the obtained "rat JTT-1 antigen" and the deduced amino acid sequence are shown in SEQ ID NO:6 and SEQ ID NO:15, respectively. The amino acid sequence (SEQ ID NO:6 or SEQ ID NO:15) deduced from the obtained cDNA sequence was compared with the amino acid sequence (SEQ ID NO:4 or SEQ ID NO:13) deduced from the obtained cDNA sequence encoding "rat JTT-1 antigen" cloned in Example 7 (Figure 14). As shown in Figure 14, the amino acid sequence encoded by the cDNA cloned in this test was completely the same as that encoded by the cDNA encoding "rat JTT-1 antigen" obtained in Example 7, except that (1) C-terminal three continuous amino acid residues (Met-Thr-Ser) changes into Thr-Ala-Pro, and [that] (2) subsequent to the Thr-Ala-Pro, 16 continuous amino acid residues (Leu-Arg-Ala-Leu-Gly-Arg-Gly-Glu-His-Ser-Ser-Cys-Gln-Asp-Arg-Asn) (SEQ ID NO:24) are added. This indicates that the cDNA cloned in this test encodes [the] an alternative splicing variant of "rat JTT-1 antigen" obtained in Example 7.

The paragraph beginning at page 105, line 21, has been amended as follows:

In order to amplify the cDNA encoding the extracellular region of "rat JTT-1 antigen" by PCR, a 5' primer having an XhoI restriction site (5'-CTGCTCGAGATGAAGCCCTACTTCTCG-3', SEQ ID NO:7) and a 3' primer having BamHI restriction site (5'-ACCCTACGGGTAACGGATCCTTCAGCTGGCAA-3', SEQ ID NO:8) at their [terminus] termini were designed and synthesized. Using cDNA clone "T132A7" obtained in Example 7 encoding the full length of "rat JTT-1 antigen" as a template, PCR was performed with the primers to prepare [the] a cDNA comprising the cDNA encoding the

extracellular region of "rat JTT-1 antigen" having XhoI and BamHI restriction sites at its [both] ends. The PCR products so obtained were digested with XhoI and BamHI and separated by agarose gel electrophoresis to isolate an about 450-bp band predicted to be the cDNA fragment encoding a desired extracellular region. The isolated cDNA fragment was subcloned into pBluescript II SK (+) (Stratagene) cleaved with XhoI and BamHI. Sequence analysis with an automated fluorescence DNA sequencer (Applied Biosystems) revealed that the cDNA fragment comprises the region encoding an amino acid sequence corresponding to [the] amino acid residues 1 to 141 of "rat JTT-1 antigen" (SEQ ID NO:4 or SEQ ID NO:13).

In the claims:

Claims 1 to 36 have been cancelled.

New claims 37 to 214 were added.

In the abstract:

[Novel cell surface molecules recognized by monoclonal antibodies against a cell surface molecule of lymphocytic cells that play an important role in autoimmune diseases and allergic diseases have been isolated, identified, and analyzed for their functions. The cell surface molecules are expressed specifically in thymocytes, lymphocytes activated by ConA-stimulation, and peripheral blood lymphocytes, and induce cell adhesion. Antibodies against the cell surface molecules significantly ameliorate pathological conditions of autoimmune diseases and allergic diseases.] A cell surface molecule that is expressed specifically in thymocytes, lymphocytes activated by ConA-stimulation, and peripheral blood lymphocytes. This molecule is involved in signal transmission of the secondary signal (costimulatory signal) essential for the activation of lymphocytes such as T cells and regulates functions of activated lymphocytes such as activated T cells. Disclosed are an antibody or a portion thereof, which binds to a polypeptide of the cell surface molecule, a polypeptide fragment thereof, or a fusion polypeptide comprising the fragment; a cell secreting the antibody or its portion; a pharmaceutical composition comprising the antibody; and methods of using the compositions for therapeutic, diagnostic and/or experimental purpose.